

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:03:31 ; Search time 21 Seconds
(without alignments)
1254.772 Million cell updates/sec

Title: US-09-806-536A-14
Perfect score: 274
Sequence: 1 MAAAEPSRRVGVGAGRMA.....AATMSAVEAATCEAKELSRK 274

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 10

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%	No.	Score	Match	Length	DB	ID	Description

No matches found

Search completed: January 13, 2004, 12:07:12
Job time : 21 secs

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 11:37:27 ; Search time 92 Seconds
(without alignments;
6419.246 Million cell updates/sec

Title: US-09-806-536A-29
Perfect score: 1338
Sequence: 1 ggtgagcgagctgtccga.....ggggcagcagcatatggggt 1338

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Prad. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: January 14, 2004, 14:03:19
Job time : 93 secs

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:05:47 ; Search time 22 Seconds
(without alignments)
876.109 Million cell updates/sec

Title: US-09-806-536A-14
Perfect score: 274
Sequence: 1 MAABPSPRRVGVGGRWA.....AATMSAVEATCAKELSRK 274

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 345061 seqs, 70344558 residues

Word size : 10

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending Patents AA New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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No matches found

Search completed: January 13, 2004, 12:11:34
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:04:22 ; Search time 21 Seconds
(without alignments)
552.056 Million cell updates/sec

Title: US-09-806-536A-14
Perfect score: 274
Sequence: 1 MAAAPSPRRVGVGGRMA.....AATWSAVEAATCRAKELSRX 274

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 10

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/ECTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description

No matches found

Search completed: January 13, 2004, 12:07:47
Job time : 21 secs

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:02:21 ; Search time 18 Seconds
(without alignments)
715.851 Million cell updates/sec

Title: US-09-806-536A-14
Perfect score: 274
Sequence: 1 MAARPEPRRVGVGVGRMA.....ANTMSAVEATCRKELSRK 274

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47036705 residues

Word size : 10

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%	No.	Score	Match	Length	DB	ID	Description

No matches found

Search completed: January 13, 2004, 12:05:43
Job time : 18 secs